

PCT09

## RAW SEQUENCE LISTING

DATE: 08/14/2001

PATENT APPLICATION: US/09/890,688

TIME: 11:01:23

Input Set : A:\Sequence Listing Kato et al.txt

Output Set: N:\CRF3\08142001\I890688.raw

3 <110> APPLICANT: Seishi KATO  
 4 Chikashi EGUCHI  
 5 Mihoro SAEKI  
 7 <120> TITLE OF INVENTION: Human Proteins and cDNAs thereof  
 9 <130> FILE REFERENCE: 2001-1102A/WMC/00653  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/890,688  
 C--> 12 <141> CURRENT FILING DATE: 2001-08-06  
 14 <150> PRIOR APPLICATION NUMBER: JP 11-346863  
 15 <151> PRIOR FILING DATE: 1999-12-06  
 17 <150> PRIOR APPLICATION NUMBER: JP 11-34684  
 18 <151> PRIOR FILING DATE: 1999-12-06  
 20 <150> PRIOR APPLICATION NUMBER: JP 2000-31062  
 21 <151> PRIOR FILING DATE: 2000-02-08  
 23 <150> PRIOR APPLICATION NUMBER: JP 2000-34091  
 24 <151> PRIOR FILING DATE: 2000-02-10  
 26 <150> PRIOR APPLICATION NUMBER: JP 2000-34090  
 27 <151> PRIOR FILING DATE: 2000-02-10  
 29 <150> PRIOR APPLICATION NUMBER: JP 2000-35829  
 30 <151> PRIOR FILING DATE: 2000-02-14  
 32 <150> PRIOR APPLICATION NUMBER: JP 2000-35899  
 33 <151> PRIOR FILING DATE: 2000-02-14  
 35 <150> PRIOR APPLICATION NUMBER: JP 2000-71161  
 36 <151> PRIOR FILING DATE: 2000-03-14  
 38 <150> PRIOR APPLICATION NUMBER: JP 2000-160851  
 39 <151> PRIOR FILING DATE: 2000-05-30  
 41 <160> NUMBER OF SEQ ID NOS: 160  
 43 <170> SOFTWARE: PatentIn Ver. 2.1  
 45 <210> SEQ ID NO: 1  
 46 <211> LENGTH: 1323  
 47 <212> TYPE: DNA  
 48 <213> ORGANISM: Homo sapiens  
 50 <220> FEATURE:  
 51 <221> NAME/KEY: CDS  
 52 <222> LOCATION: (27)..(881)  
 54 <400> SEQUENCE: 1  
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 56 Met Ala Ala Pro Gly Leu Arg Leu Gly  
 57 1 5  
 59 gcg gga aga ctc ttt gaa atg cct gcg gtg cta gag cga ctg agc cgc 101  
 60 Ala Gly Arg Leu Phe Glu Met Pro Ala Val Leu Arg Leu Ser Arg  
 61 10 15 20 25  
 63 tat aat agc acg tcc caa gct ttt gct gag gtg ctg cgg ctg ccg aag 149  
 64 Tyr Asn Ser Thr Ser Gln Ala Phe Ala Glu Val Leu Arg Leu Pro Lys  
 65 30 35 40  
 67 cag cag ctg agg aag ctg ctg tac ccg ctg cag gaa gta gag cgg ttc 197  
 68 Gln Gln Leu Arg Lys Leu Leu Tyr Pro Leu Gln Glu Val Glu Arg Phe  
 69 45 50 55

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71 ctc gcc ccc tac ggg agg caa gac ctt cac ctg cgt atc ttt gac cca 245
72 Leu Ala Pro Tyr Gly Arg Gln Asp Leu His Leu Arg Ile Phe Asp Pro
73          60          65          70
75 agc ccg gag gac ata gcc agg gcg gac aac atc ttc acg gcc act gaa 293
76 Ser Pro Glu Asp Ile Ala Arg Ala Asp Asn Ile Phe Thr Ala Thr Glu
77          75          80          85
79 cgg aac cgc atc gac tac gtc agc tcc gcc gtc cgt atc gac cac gcc 341
80 Arg Asn Arg Ile Asp Tyr Val Ser Ser Ala Val Arg Ile Asp His Ala
81 90          95          100          105
83 ccg gac ctt ccg cgg cca gag gtg tgt ttt ata ggc aga agc aat gtt 389
84 Pro Asp Leu Pro Arg Pro Glu Val Cys Phe Ile Gly Arg Ser Asn Val
85          110          115          120
87 gga aaa tca tct cta atc aag gct tta ttt tca ctg gcc cct gag gtt 437
88 Gly Lys Ser Ser Leu Ile Lys Ala Leu Phe Ser Leu Ala Pro Glu Val
89          125          130          135
91 gaa gtc aga gtc tcc aaa aaa cca gga cac aca aag aaa atg aat ttt 485
92 Glu Val Arg Val Ser Lys Lys Pro Gly His Thr Lys Lys Met Asn Phe
93          140          145          150
95 ttc aaa gtt gga aaa cat ttt aca gtg gtg gac atg cca ggt tat ggc 533
96 Phe Lys Val Gly Lys His Phe Thr Val Val Asp Met Pro Gly Tyr Gly
97          155          160          165
99 ttt aga gca cct gaa gat ttt gtt gac atg gta gag acc tat cta aaa 581
100 Phe Arg Ala Pro Glu Asp Phe Val Asp Met Val Glu Thr Tyr Leu Lys
101 170          175          180          185
103 gaa cga agg aac ttg aag aga aca ttt tta tta gtg gat agc gtt gtt 629
104 Glu Arg Arg Asn Leu Lys Arg Thr Phe Leu Leu Val Asp Ser Val Val
105          190          195          200
107 gga att caa aaa aca gac aat att gcc ata gaa atg tgt gaa gaa ttt 677
108 Gly Ile Gln Lys Thr Asp Asn Ile Ala Ile Glu Met Cys Glu Glu Phe
109          205          210          215
111 gca tta cct tat gtg att gta tta aca aaa att gac aaa tct tcc aag 725
112 Ala Leu Pro Tyr Val Ile Val Leu Thr Lys Ile Asp Lys Ser Ser Lys
113          220          225          230
115 gga cat ctt tta aaa caa gtg ctt cag atc cag aaa ttt gtt aac atg 773
116 Gly His Leu Leu Lys Gln Val Leu Gln Ile Gln Lys Phe Val Asn Met
117          235          240          245
119 aaa act caa gga tgt ttt cct cag ttg ttt cct gta agt gct gtg acc 821
120 Lys Thr Gln Gly Cys Phe Pro Gln Leu Phe Pro Val Ser Ala Val Thr
121 250          255          260          265
123 ttt tct gga atc cac ctg ttg aga tgc ttt ata gcc agt gta aca gga 869
124 Phe Ser Gly Ile His Leu Leu Arg Cys Phe Ile Ala Ser Val Thr Gly
125          270          275          280
127 agt ctt gac taa tgggtcccg ttttagctgaa gattcaaaag ctttatgcta 921
128 Ser Leu Asp
131 actggagtta aatacctaga agaatttcaa cattgtttta aatgttgtgc atctgtaact 981
133 tcaggaggat cacttgagct ttaaaacctg tgccttctcg aaacaagaat ttgtgcctga 1041
135 ggtgaaaaaa gtttgtaagt tattgaatta tgggtttcat tagaacagct actagctgat 1101
137 tccccatatt taacaaactg acaagagcac atccataaaa tgaaaacctg ttacaactat 1161
139 gtacagaagg gtttgacgtt ttattgggct tttgtctttt aaagaatatg tctactatgg 1221

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141 gtattttttt tttaaatgtt aaaatgggct aggtaaaagg gggctgcttt tctgttaagc 1281
143 atcgataggt aagttgatgg ataaaagtta ctatgtaagc ct 1323
146 <210> SEQ ID NO: 2
147 <211> LENGTH: 284
148 <212> TYPE: PRT
149 <213> ORGANISM: Homo sapiens
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153 1 5 10 15
155 Pro Ala Val Leu Glu Arg Leu Ser Arg Tyr Asn Ser Thr Ser Gln Ala
156 20 25 30
158 Phe Ala Glu Val Leu Arg Leu Pro Lys Gln Gln Leu Arg Lys Leu Leu
159 35 40 45
161 Tyr Pro Leu Gln Glu Val Glu Arg Phe Leu Ala Pro Tyr Gly Arg Gln
162 50 55 60
164 Asp Leu His Leu Arg Ile Phe Asp Pro Ser Pro Glu Asp Ile Ala Arg
165 65 70 75 80
167 Ala Asp Asn Ile Phe Thr Ala Thr Glu Arg Asn Arg Ile Asp Tyr Val
168 85 90 95
170 Ser Ser Ala Val Arg Ile Asp His Ala Pro Asp Leu Pro Arg Pro Glu
171 100 105 110
173 Val Cys Phe Ile Gly Arg Ser Asn Val Gly Lys Ser Ser Leu Ile Lys
174 115 120 125
176 Ala Leu Phe Ser Leu Ala Pro Glu Val Glu Val Arg Val Ser Lys Lys
177 130 135 140
179 Pro Gly His Thr Lys Lys Met Asn Phe Phe Lys Val Gly Lys His Phe
180 145 150 155 160
182 Thr Val Val Asp Met Pro Gly Tyr Gly Phe Arg Ala Pro Glu Asp Phe
183 165 170 175
185 Val Asp Met Val Glu Thr Tyr Leu Lys Glu Arg Arg Asn Leu Lys Arg
186 180 185 190
188 Thr Phe Leu Leu Val Asp Ser Val Val Gly Ile Gln Lys Thr Asp Asn
189 195 200 205
191 Ile Ala Ile Glu Met Cys Glu Glu Phe Ala Leu Pro Tyr Val Ile Val
192 210 215 220
194 Leu Thr Lys Ile Asp Lys Ser Ser Lys Gly His Leu Leu Lys Gln Val
195 225 230 235 240
197 Leu Gln Ile Gln Lys Phe Val Asn Met Lys Thr Gln Gly Cys Phe Pro
198 245 250 255
200 Gln Leu Phe Pro Val Ser Ala Val Thr Phe Ser Gly Ile His Leu Leu
201 260 265 270
203 Arg Cys Phe Ile Ala Ser Val Thr Gly Ser Leu Asp
204 275 280
207 <210> SEQ ID NO: 3
208 <211> LENGTH: 1120
209 <212> TYPE: DNA
210 <213> ORGANISM: Homo sapiens
212 <220> FEATURE:
213 <221> NAME/KEY: CDS

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214 <222> LOCATION: (18)..(719)
216 <400> SEQUENCE: 3
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218 Met Ala Ala Pro Val Val Thr Ala Pro Gly Arg
219 1 5 10
221 gct ctg ctg cgg gcg ggc gct gga cgg ctg ctt cgg gga ggc gtc cag 98
222 Ala Leu Leu Arg Ala Gly Ala Gly Arg Leu Leu Arg Gly Gly Val Gln
223 15 20 25
225 gag cta ctg cgg ccg cga cat gaa ggg aac gcc cct gac ctg gcc tgc 146
226 Glu Leu Leu Arg Pro Arg His Glu Gly Asn Ala Pro Asp Leu Ala Cys
227 30 35 40
229 aac ttc agc ctt tct caa aat cgg ggc acg gtc atc gtg gag cgc tgg 194
230 Asn Phe Ser Leu Ser Gln Asn Arg Gly Thr Val Ile Val Glu Arg Trp
231 45 50 55
233 tgg aag gta ccg ctg gcc ggg ggg ggc cgg aag ccg cgc ctg cac cgg 242
234 Trp Lys Val Pro Leu Ala Gly Gly Gly Arg Lys Pro Arg Leu His Arg
235 60 65 70 75
237 cga cat cgc gtc tat aag ctg gtg gag gac acg aag cat cgg ccc aaa 290
238 Arg His Arg Val Tyr Lys Leu Val Glu Asp Thr Lys His Arg Pro Lys
239 80 85 90
241 gaa aac ctg gag ctc atc ctg acg cag tcg gtg gag aat gtt gga gtc 338
242 Glu Asn Leu Glu Leu Ile Leu Thr Gln Ser Val Glu Asn Val Gly Val
243 95 100 105
245 cgg ggt gac ctg gtc tca gtg aag aaa tct tta ggc cgg aat cga ctc 386
246 Arg Gly Asp Leu Val Ser Val Lys Lys Ser Leu Gly Arg Asn Arg Leu
247 110 115 120
249 ctt cct cag gga ctg gct gta tat gca tcc cct gaa aac aag aag ctg 434
250 Leu Pro Gln Gly Leu Ala Val Tyr Ala Ser Pro Glu Asn Lys Lys Leu
251 125 130 135
253 ttt gaa gag gag aaa ttg ctg aga caa gaa gga aaa tta gag aag atc 482
254 Phe Glu Glu Glu Lys Leu Leu Arg Gln Glu Gly Lys Leu Glu Lys Ile
255 140 145 150 155
257 cag acc aag gca ggt gag gcg ctt ggt gtt gtg gtt gcc cca cat aca 530
258 Gln Thr Lys Ala Gly Glu Ala Leu Gly Val Val Val Ala Pro His Thr
259 160 165 170
261 tta aag tta cca gca gag cct atc aca cgg tgg ggc gag tat tgg tgt 578
262 Leu Lys Leu Pro Ala Glu Pro Ile Thr Arg Trp Gly Glu Tyr Trp Cys
263 175 180 185
265 gag gtg acg gta aat ggg ctt gat act gtg aga gtg cct atg tct gtc 626
266 Glu Val Thr Val Asn Gly Leu Asp Thr Val Arg Val Pro Met Ser Val
267 190 195 200
269 gtg aac ttt gag aag ccc aag acc aaa aga tat aag tac tgg tta gcc 674
270 Val Asn Phe Glu Lys Pro Lys Thr Lys Arg Tyr Lys Tyr Trp Leu Ala
271 205 210 215
273 cag caa gct gcc aag gct atg gcc ccc acc agc ccc cag atc taa 719
274 Gln Gln Ala Ala Lys Ala Met Ala Pro Thr Ser Pro Gln Ile
275 220 225 230
277 atctactctc cctccaaggc agcaaagcag aatcgggagc agtggagcag aaatgtgcaa 779
279 gcaccctgat ctactccca gctctgacca aatacagaat tttagagaac atctgaagac 839

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281 atcagactgc actgcgtata catgttgaat tcttcatttt tgccatcttt aactgtcatc 899
283 actggggcag ggaagtcctg ttccagaagt accaggctgt agatttgata agctagatgc 959
285 agtagaccga aaccatccaa aacctgttta gcttcttcct ccattggagt ttattgggac 1019
287 aaacaggaga gccagccatt gtctccagta cttgcctcat tctcatcatc caaactgaac 1079
289 atttgatatcc caagcagaaa taaagagaat atgttctttt t 1120
292 <210> SEQ ID NO: 4
293 <211> LENGTH: 233
294 <212> TYPE: PRT
295 <213> ORGANISM: Homo sapiens
297 <400> SEQUENCE: 4
298 Met Ala Ala Pro Val Thr Ala Pro Gly Arg Ala Leu Leu Arg Ala
299 1 5 10 15
301 Gly Ala Gly Arg Leu Leu Arg Gly Gly Val Gln Glu Leu Leu Arg Pro
302 20 25 30
304 Arg His Glu Gly Asn Ala Pro Asp Leu Ala Cys Asn Phe Ser Leu Ser
305 35 40 45
307 Gln Asn Arg Gly Thr Val Ile Val Glu Arg Trp Trp Lys Val Pro Leu
308 50 55 60
310 Ala Gly Gly Gly Arg Lys Pro Arg Leu His Arg Arg His Arg Val Tyr
311 65 70 75 80
313 Lys Leu Val Glu Asp Thr Lys His Arg Pro Lys Glu Asn Leu Glu Leu
314 85 90 95
316 Ile Leu Thr Gln Ser Val Glu Asn Val Gly Val Arg Gly Asp Leu Val
317 100 105 110
319 Ser Val Lys Lys Ser Leu Gly Arg Asn Arg Leu Leu Pro Gln Gly Leu
320 115 120 125
322 Ala Val Tyr Ala Ser Pro Glu Asn Lys Lys Leu Phe Glu Glu Glu Lys
323 130 135 140
325 Leu Leu Arg Gln Glu Gly Lys Leu Glu Lys Ile Gln Thr Lys Ala Gly
326 145 150 155 160
328 Glu Ala Leu Gly Val Val Val Ala Pro His Thr Leu Lys Leu Pro Ala
329 165 170 175
331 Glu Pro Ile Thr Arg Trp Gly Glu Tyr Trp Cys Glu Val Thr Val Asn
332 180 185 190
334 Gly Leu Asp Thr Val Arg Val Pro Met Ser Val Val Asn Phe Glu Lys
335 195 200 205
337 Pro Lys Thr Lys Arg Tyr Lys Tyr Trp Leu Ala Gln Gln Ala Ala Lys
338 210 215 220
340 Ala Met Ala Pro Thr Ser Pro Gln Ile
341 225 230
344 <210> SEQ ID NO: 5
345 <211> LENGTH: 528
346 <212> TYPE: DNA
347 <213> ORGANISM: Homo sapiens
349 <220> FEATURE:
350 <221> NAME/KEY: CDS
351 <222> LOCATION: (90)..(284)
353 <400> SEQUENCE: 5
354 aaggaaattg acgaacacgt gacgcggtcg ggcggaccac tgcagactga gcggtggacc 60

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VERIFICATION SUMMARY

DATE: 08/14/2001

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TIME: 11:01:24

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:6698 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:105  
L:6708 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:105  
L:6735 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:106  
L:6740 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:106